

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 27, 2004, 14:01:10 ; Search time 8 Seconds
(without alignments)

3.501 Million cell updates/sec

Title: US-10-619-220-1

Perfect score: 2551

Sequence: 1 gcaagtgacacacagtg.....taaaagtaagtaataaata 2551

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 274 seqs, 5490 residues

Total number of hits satisfying chosen parameters: 548

Minimum DB seq length: 8

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 279 summaries

Database : rge1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	39.4	1.5	45	1	AR194144
C 2	38.4	1.5	45	1	AR194143
C 3	37.4	1.5	43	1	E23361
C 4	34.6	1.4	41	1	I58616
C 5	34.6	1.4	41	1	I63514
C 6	33	1.3	41	1	I58615
C 7	33	1.3	41	1	I63513
C 8	32	1.3	32	1	AR090265
C 9	32	1.3	32	1	AR197300
C 10	32	1.3	32	1	AR259454
C 11	31	1.2	31	1	AR432290
C 12	30.4	1.2	32	1	AR090266
C 13	30.4	1.2	32	1	AR197301
C 14	29	1.1	29	1	AR259455
C 15	29	1.1	29	1	AR432288
C 16	27	1.1	27	1	I58624
C 17	27	1.1	27	1	I63522
C 18	26	1.0	26	1	I58623
C 19	26	1.0	26	1	I63521
C 20	26	1.0	26	1	AR432289
C 21	25	1.0	30	1	AX821872
C 22	24	0.9	24	1	AR050854
C 23	24	0.9	24	1	BD218038
C 24	24	0.9	24	1	I40368
C 25	24	0.9	24	1	AR194107
C 26	24	0.9	24	1	AR274264
C 27	24	0.9	28	1	AX821871
C 28	24	0.9	30	1	AX060545
C 29	23	0.9	28	1	AX060547
C 30	21	0.8	21	1	AR071978
C 31	20.8	0.8	21	1	I68115
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C 33	20	0.8	20	1	A98445

C 34	20	0.8	20	1	A98446
C 35	20	0.8	20	1	AR143112
C 36	20	0.8	20	1	AR143113
C 37	20	0.8	20	1	AR143114
C 38	20	0.8	20	1	AR143115
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C 96	20	0.8	20	1	AR432224
C 97	20	0.8	20	1	AR432225
C 98	20	0.8	20	1	AR432226
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C 110	20	0.8	20	1	AR432318	183	14.4	0.6	17	1	AX325717	ACCESSION:AX325717
C 111	20	0.8	20	1	AR432319	184	14.4	0.6	17	1	AX325718	ACCESSION:AX325718
C 112	20	0.8	20	1	AR432320	185	14.4	0.6	17	1	AX649037	ACCESSION:AX649037
C 113	20	0.8	20	1	AR432321	186	14.4	0.6	17	1	AX649038	ACCESSION:AX649038
C 114	20	0.8	20	1	AR432322	187	14.4	0.6	17	1	AX672697	ACCESSION:AX672697
C 115	20	0.8	20	1	AR432323	188	14.4	0.6	17	1	AX722552	ACCESSION:AX722552
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C 161	16.8	0.7	20	1	AR432270	234	13.8	0.5	17	1	AX326226	ACCESSION:AX326226
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ALIGMENTS

RESULT 1

AR194144/c

LOCUS

DEFINITION

SEQUENCE 87 from patent US 6348334.

ACCESSION

AR194144

VERSION

AR194144.1 GI:20240736

KEYWORDS

SOURCE

ORGANISM

Unknown.

REFERENCE

1 (bases 1 to 45)

AUTHORS

Nagata,S., Suda,T., Takahashi,T. and Nakamura,N.

TITLE

DNA encoding Fas ligand

JOURNAL

Patent: US 6348334-A 87 19-FEB-2002;

FEATURES

source

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Query Match

Best Local Similarity

1.5%; Score 39.4; DB 1; Length 45;

Matches 40; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy

218 ACCATGCTGGCATCTGGACCTCTACCTCTGTTCTTAC 258

Db

44 ACCATGCTGGCATCTGGACCTCTACCTCTGTTCTTAC 4

JOURNAL

Patent: US 6348334-A 86 19-FEB-2002;

FEATURES

source

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Query Match

Best Local Similarity

1.5%; Score 38.4; DB 1; Length 45;

Matches 39; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy

218 ACCATGCTGGCATCTGGACCTCTACCTCTGTTCTTAC 257

Db

6 ACCATGCTGGCATCTGGACCTCTACCTCTGTTCTTAC 45

RESULT 3

E23361/c

LOCUS

DEFINITION

Virus vector system expressing apoptosis-related gene.

ACCESSION

E23361

VERSION

E23361.1 GI:13024384

KEYWORDS

JP 1999075859-A/7.

SOURCE

unidentified

ORGANISM

unclassified.

REFERENCE

1 (bases 1 to 43)

AUTHORS

Hirofumi,H.

TITLE

Virus vector system expressing apoptosis-related gene

JOURNAL

Patent: JP 1999075859-A 7 23-MAR-1999;

COMMENT

R B JENSEN KK

OS

Unidentified

PN

JP 1999075859-A/7

PD

23-MAR-1999

PF

08-SEP-1997 JP 1997259235

PR

HIROFUMI HANADA

PC

CI2N15/09, CI2N5/10, CI2N7/00/A61K35/76, A61K48/00, (CI2N5/10, PC

CI2N1/91),

PC

(CI2N7/00, CI2N1/92), CI2N15/00, CI2N5/00, (CI2N5/00, CI2N1/91) CC

Strandedness: Single;

CC

Topology: Linear;

PH

Key

Location/Qualifiers

FT

source

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Query Match

Best Local Similarity

1.5%; Score 37.4; DB 1; Length 43;

Matches 38; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy

1193 TCACACTTCAGAAATGCAATCCAAAGCTTGGTCTAGAGT 1231

Db

43 TCACACTTCAGAAATGCAATCCAAAGCTTGGTCTAGAGT 5

RESULT 4

I58616/c

LOCUS

DEFINITION

Sequence 2 from patent US 5652210.

ACCESSION

I58616

VERSION

I58616.1 GI:2477854

KEYWORDS

Unknown.

SOURCE

Unknown.

ORGANISM

Unclassified.

REFERENCE

1 (bases 1 to 41)

AUTHORS

Barr,P.J., Shapiro,J.P. and Kiefer,M.C.

TITLE

Splice variant of the Fas (APO-1) antigen, Fas.DELTA.TM

JOURNAL

Patent: US 5652210-A 2 29-JUL-1997;

ALIGMENTS

RESULT 2

AR194143

LOCUS

DEFINITION

SEQUENCE 86 from patent US 6348334.

ACCESSION

AR194143

VERSION

AR194143.1 GI:20240735

KEYWORDS

SOURCE

Unknown.

ORGANISM

Unknown.

REFERENCE

1 (bases 1 to 45)

AUTHORS

Nagata,S., Suda,T., Takahashi,T. and Nakamura,N.

TITLE

DNA encoding Fas ligand

JOURNAL

Patent: US 6348334-A 86 19-FEB-2002;

FEATURES

source

1..45

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Query Match

Best Local Similarity

1.5%; Score 37.4; DB 1; Length 43;

Matches 38; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy

1193 TCACACTTCAGAAATGCAATCCAAAGCTTGGTCTAGAGT 1231

Db

43 TCACACTTCAGAAATGCAATCCAAAGCTTGGTCTAGAGT 5

RESULT 4

I58616/c

LOCUS

DEFINITION

Sequence 2 from patent US 5652210.

ACCESSION

I58616

VERSION

I58616.1 GI:2477854

KEYWORDS

Unknown.

SOURCE

Unknown.

ORGANISM

Unclassified.

REFERENCE

1 (bases 1 to 41)

AUTHORS

Barr,P.J., Shapiro,J.P. and Kiefer,M.C.

TITLE

Splice variant of the Fas (APO-1) antigen, Fas.DELTA.TM

JOURNAL

Patent: US 5652210-A 2 29-JUL-1997;

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OM nucleic - nucleic search, using sw model

Run on: October 27, 2004, 14:03:45 ; Search time 13 Seconds
(without alignments)

3.708 Million cell updates/sec

Title: US-10-619-220-1

Perfect score: 2551
Sequence: 1 gcaaggtgacacacaggtg.....taaaagtagtaataaata 2551

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 471 seqs, 9448 residues

Total number of hits satisfying chosen parameters: 942

Minimum DB seq length: 8

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 472 summaries

Database : rngl.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	2.0	50	1	Human leukocyte ge
2	50	2.0	50	1	Human leukocyte ge
3	39.4	1.5	45	1	Human Fas ligand g
4	38.4	1.5	45	1	Human Fas ligand g
5	37.4	1.5	43	1	Human Fas PCR prim
6	34.6	1.4	41	1	Fas-delta-TM 3', pr
7	33	1.3	41	1	Fas-delta-TM 5', pr
8	32	1.3	32	1	Human gene specifi
9	31	1.2	31	1	Human Fas probe.
10	31	1.2	31	1	Probe for human Fa
11	31	1.2	31	1	Human Fas probe se
12	30.6	1.2	31	1	Human gene single
13	30.6	1.2	31	1	Human gene single
14	30.4	1.2	32	1	PCR primer to ampl
15	30	1.2	30	1	Human Fas forward
16	29	1.1	29	1	Human Fas PCR prim
17	29	1.1	29	1	Human Fas PCR prim
18	29	1.1	29	1	Human Fas reverse
19	27	1.1	27	1	Human Fas cDNA, PC
20	26	1.0	26	1	Human Fas PCR prim
21	26	1.0	26	1	Human Fas cDNA, PC
22	26	1.0	26	1	Human Fas PCR prim
23	26	1.0	26	1	Human Fas cDNA, PC
24	25	1.0	24	1	Human Fas antigen
25	24	0.9	24	1	Human Fas antigen
26	24	0.9	24	1	Human Fas antigen
27	24	0.9	24	1	Human Fas extracel
28	24	0.9	24	1	Human Fas antigen
29	24	0.9	24	1	PCR primer for huf
30	24	0.9	24	1	PCR primer for huf
31	24	0.9	24	1	Cancer detection m
32	24	0.9	24	1	PCR primer to ampl
33	24	0.9	24	1	Human Fas antigen
					PCR primer for chi

C 34	24	0.9	30	1	AAA91134	PCR primer for chi
C 35	24	0.9	30	1	AAA91136	PCR primer for chi
C 36	23	0.9	23	1	ABN85357	Fas antigen relate
C 37	23	0.9	23	1	ABN85358	Fas antigen relate
C 38	23	0.9	23	1	ABN85359	Fas antigen relate
C 39	23	0.9	28	1	AAA91137	PCR primer for chi
C 40	22	0.9	22	1	AAT10246	Human Fas antigen
C 41	22	0.9	22	1	AAA27546	Fas ligand promote
C 42	22	0.9	22	1	ADA43788	Human TNFRSF6 PCR
C 43	22	0.9	22	1	ADA43745	Human TNFRSF6 PCR
C 44	22	0.9	22	1	ADA43785	Human neurodegener
C 45	22	0.9	22	1	ADH54263	Human neurodegener
C 46	22	0.9	22	1	ADH54262	Human neurodegener
C 47	22	0.9	22	1	ADH54266	Human Fas antigen
C 48	21	0.8	21	1	AAT34532	Fas cell surface r
C 49	21	0.8	21	1	ABA02997	Human TNFRSF6 sequ
C 50	21	0.8	21	1	ADA43787	Cancer detection m
C 51	21	0.8	21	1	ADG89317	Human neurodegener
C 52	21	0.8	21	1	ADH54265	PCR primer to ampl
C 53	21	0.8	21	1	ADP27795	Fas bait protein (
C 54	20.8	0.8	24	1	AAT43761	Fas bait protein (
C 55	20.8	0.8	24	1	AAT43761	PCR primer 82689.
C 56	20	0.8	20	1	AA22801	PCR primer 82690.
C 57	20	0.8	20	1	AA22802	Antisense oligonuc
C 58	20	0.8	20	1	AA22803	Antisense oligonuc
C 59	20	0.8	20	1	AA22804	Antisense oligonuc
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C 106	20	0.8	20	1	AA22851	Antisense oligonuc

C 107	20	0.8	20	1	ABN79722	Human Fas target o	C 180	20	0.8	20	1	ADL27762	Human Fas cDNA, an
C 108	20	0.8	20	1	ABN79734	Human Fas target o	C 181	20	0.8	20	1	ADL27776	Human Fas cDNA, an
C 109	20	0.8	20	1	ABN79693	Human Fas target o	C 182	20	0.8	20	1	ADL27747	Human Fas cDNA, an
C 110	20	0.8	20	1	ABN79708	Human Fas target o	C 183	20	0.8	20	1	ADL27765	Human Fas cDNA, an
C 111	20	0.8	20	1	ABN79730	Human Fas target o	C 184	20	0.8	20	1	ADL27782	Human Fas cDNA, an
C 112	20	0.8	20	1	ABN79717	Human Fas target o	C 185	20	0.8	20	1	ADL27791	Human Fas cDNA, an
C 113	20	0.8	20	1	ABN79607	Human Fas chimeric	C 186	20	0.8	20	1	ADL27651	Human Fas cDNA, an
C 114	20	0.8	20	1	ABN79609	Human Fas chimeric	C 187	20	0.8	20	1	ADL27759	Human Fas cDNA, an
C 115	20	0.8	20	1	ABN79721	Human Fas target o	C 188	20	0.8	20	1	ADL27760	Human Fas cDNA, an
C 116	20	0.8	20	1	ABN79589	Human Fas chimeric	C 189	20	0.8	20	1	ADL27763	Human Fas cDNA, an
C 117	20	0.8	20	1	ABN79604	Human Fas chimeric	C 190	20	0.8	20	1	ADL27773	Human Fas cDNA, an
C 118	20	0.8	20	1	ABN79715	Human Fas target o	C 191	20	0.8	20	1	ADL27777	Human Fas cDNA, an
C 119	20	0.8	20	1	ABN79733	Human Fas target o	C 192	20	0.8	20	1	ADL27788	Human Fas cDNA, an
C 120	20	0.8	20	1	ABN79735	Human Fas target o	C 193	20	0.8	20	1	ADL27652	Human Fas cDNA, an
C 121	20	0.8	20	1	ABN79597	Human Fas chimeric	C 194	20	0.8	20	1	ADL27657	Human Fas cDNA, an
C 122	20	0.8	20	1	ABN79602	Human Fas chimeric	C 195	20	0.8	20	1	ADL27748	Human Fas cDNA, an
C 123	20	0.8	20	1	ABN79593	Human Fas chimeric	C 196	20	0.8	20	1	ADL27752	Human Fas cDNA, an
C 124	20	0.8	20	1	ABN79601	Human Fas chimeric	C 197	20	0.8	20	1	ADL27754	Human Fas cDNA, an
C 125	20	0.8	20	1	ABN79692	Human Fas target o	C 198	20	0.8	20	1	ADL27756	Human Fas cDNA, an
C 126	20	0.8	20	1	ABN79700	Human Fas target o	C 199	20	0.8	20	1	ADL27660	Human Fas cDNA, an
C 127	20	0.8	20	1	ABN79732	Human Fas target o	C 200	20	0.8	20	1	ADL27770	Human Fas cDNA, an
C 128	20	0.8	20	1	ABN79594	Human Fas chimeric	C 201	20	0.8	20	1	ADL27645	Human Fas cDNA, an
C 129	20	0.8	20	1	ABN79603	Human Fas chimeric	C 202	20	0.8	20	1	ADL27751	Human Fas cDNA, an
C 130	20	0.8	20	1	ABN79711	Human Fas target o	C 203	20	0.8	20	1	ADL27757	Human Fas cDNA, an
C 131	20	0.8	20	1	ABN79713	Human Fas target o	C 204	20	0.8	20	1	ADL27767	Human Fas cDNA, an
C 132	20	0.8	20	1	ABN79595	Human Fas chimeric	C 205	20	0.8	20	1	ADL27768	Human Fas cDNA, an
C 133	20	0.8	20	1	ABN79596	Human Fas chimeric	C 206	20	0.8	20	1	ADL27779	Human Fas cDNA, an
C 134	20	0.8	20	1	ABN79696	Human Fas target o	C 207	20	0.8	20	1	ADL27758	Human Fas cDNA, an
C 135	20	0.8	20	1	ABN79704	Human Fas target o	C 208	20	0.8	20	1	ADL27771	Human Fas cDNA, an
C 136	20	0.8	20	1	ABN79598	Human Fas chimeric	C 209	20	0.8	20	1	ADL27780	Human Fas cDNA, an
C 137	20	0.8	20	1	ABN79605	Human Fas chimeric	C 210	20	0.8	20	1	ADL27781	Human Fas cDNA, an
C 138	20	0.8	20	1	ABN79695	Human Fas target o	C 211	20	0.8	20	1	ADL27643	Human Fas cDNA, an
C 139	20	0.8	20	1	ABN79703	Human Fas target o	C 212	20	0.8	20	1	ADL27646	Human Fas cDNA, an
C 140	20	0.8	20	1	ABN79719	Human Fas target o	C 213	20	0.8	20	1	ADL27647	Human Fas cDNA, an
C 141	20	0.8	20	1	ABN79590	Human Fas chimeric	C 214	20	0.8	20	1	ADL27658	Human Fas cDNA, an
C 142	20	0.8	20	1	ABN79606	Human Fas chimeric	C 215	20	0.8	20	1	ADL27772	Human Fas cDNA, an
C 143	20	0.8	20	1	ABN79691	Human Fas target o	C 216	20	0.8	20	1	ADL27650	Human Fas cDNA, an
C 144	20	0.8	20	1	ABN79698	Human Fas target o	C 217	20	0.8	20	1	ADL27769	Human Fas cDNA, an
C 145	20	0.8	20	1	ABN79709	Human Fas target o	C 218	20	0.8	20	1	ADL27653	Human Fas cDNA, an
C 146	20	0.8	20	1	ABN79710	Human Fas target o	C 219	20	0.8	20	1	ADL27654	Human Fas cDNA, an
C 147	20	0.8	20	1	ABN79736	Human Fas target o	C 220	20	0.8	20	1	ADL27766	Human Fas cDNA, an
C 148	20	0.8	20	1	ABQ74699	FAS (APO-1) Gene a	C 221	20	0.8	20	1	ADL27778	Human Fas cDNA, an
C 149	20	0.8	20	1	ABQ74672	FAS (APO-1) Gene s	C 222	20	0.8	20	1	ADL27790	Human Fas cDNA, an
C 150	20	0.8	20	1	AL57646	RT-PCR primer RT-C	C 223	20	0.8	20	1	ADL27644	Human Fas cDNA, an
C 151	20	0.8	20	1	ACC98689	Apol PCR primer SE	C 224	20	0.8	20	1	ADL27648	Human Fas cDNA, an
C 152	20	0.8	20	1	ACH66597	Apol PCR primer SE	C 225	20	0.8	20	1	ADL27659	Human Fas cDNA, an
C 153	20	0.8	20	1	ACH66597	Sense PCR primer u	C 226	20	0.8	20	1	ADL27662	Human Fas cDNA, an
C 154	20	0.8	20	1	ADN95035	Wild type protein	C 227	20	0.8	20	1	ADL27750	Human Fas cDNA, an
C 155	20	0.8	20	1	ADE43791	Human TNFRSF6 sequ	C 228	20	0.8	20	1	ADL27783	Human Fas cDNA, an
C 156	20	0.8	20	1	ADE43790	Human TNFRSF6 sequ	C 229	20	0.8	20	1	ADL27787	Human Fas cDNA, an
C 157	20	0.8	20	1	ADE43771	Human TNFRSF6 sequ	C 230	20	0.8	20	1	ADL27642	Human Fas cDNA, an
C 158	20	0.8	20	1	ADE43794	Human TNFRSF6 sequ	C 231	20	0.8	20	1	ADL27649	Human Fas cDNA, an
C 159	20	0.8	20	1	ADE43795	Human TNFRSF6 sequ	C 232	20	0.8	20	1	ADL27774	Human Fas cDNA, an
C 160	20	0.8	20	1	ADH54268	Human neurodegener	C 233	20	0.8	20	1	ADL27755	Human Fas cDNA, an
C 161	20	0.8	20	1	ADH54269	Human neurodegener	C 234	20	0.8	20	1	ADL27775	Human Fas cDNA, an
C 162	20	0.8	20	1	ADH54273	Human neurodegener	C 235	20	0.8	20	1	ADL27786	Human Fas cDNA, an
C 163	20	0.8	20	1	ADH54249	Human neurodegener	C 236	20	0.8	20	1	ADL27792	Human Fas cDNA, an
C 164	20	0.8	20	1	ADH54272	Human neurodegener	C 237	20	0.8	20	1	ADM53422	Human Fas antisens
C 165	20	0.8	20	1	ADJ57348	Human Fas PCR prim	C 238	20	0.8	20	1	ADM53548	Human Fas antisens
C 166	20	0.8	20	1	ADJ57362	Human Fas PCR prim	C 239	20	0.8	20	1	ADM53564	Human Fas antisens
C 167	20	0.8	20	1	ADJ57347	FAS (APO-1) PCR pr	C 240	20	0.8	20	1	ADM53420	Human Fas antisens
C 168	20	0.8	20	1	ADH80318	FAS (APO-1) PCR pr	C 241	20	0.8	20	1	ADM53421	Human Fas antisens
C 169	20	0.8	20	1	ADH80380	Human Fas cDNA, an	C 242	20	0.8	20	1	ADM53426	Human Fas antisens
C 170	20	0.8	20	1	ADL27655	Human Fas cDNA, an	C 243	20	0.8	20	1	ADM53534	Human Fas antisens
C 171	20	0.8	20	1	ADL27661	Human Fas cDNA, an	C 244	20	0.8	20	1	ADM53553	Human Fas antisens
C 172	20	0.8	20	1	ADL27746	Human Fas cDNA, an	C 245	20	0.8	20	1	ADM53556	Human Fas antisens
C 173	20	0.8	20	1	ADL27789	Human Fas cDNA, an	C 246	20	0.8	20	1	ADM53418	Human Fas antisens
C 174	20	0.8	20	1	ADL27749	Human Fas cDNA, an	C 247	20	0.8	20	1	ADM53425	Human Fas antisens
C 175	20	0.8	20	1	ADL27753	Human Fas cDNA, an	C 248	20	0.8	20	1	ADM53427	Human Fas antisens
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C 177	20	0.8	20	1	ADL27784	Human Fas cDNA, an	C 250	20	0.8	20	1	ADM53520	Human Fas antisens
C 178	20	0.8	20	1	ADL27656	Human Fas cDNA, an	C 251	20	0.8	20	1	ADM53520	Human Fas antisens
C 179	20	0.8	20	1	ADL27761	Human Fas cDNA, an	C 252	20	0.8	20	1	ADM53527	Human Fas antisens

C 253	20	0.8	20	1	ADMS3538	Human Fas antisense	326	16.8	0.7	20	1	ADD25012	Human caspase-8 an
C 254	20	0.8	20	1	ADMS3545	Human Fas antisense	C 327	16.8	0.7	20	1	ADD42290	Human infertility
C 255	20	0.8	20	1	ADMS3554	Human Fas antisense	C 328	16.8	0.7	20	1	ABZ77441	PCR primer used to
C 256	20	0.8	20	1	ADMS3555	Human Fas antisense	C 329	16.8	0.7	20	1	ADJ61356	Oligonucleotide as
C 257	20	0.8	20	1	ADMS3417	Human Fas antisense	C 330	16.8	0.7	20	1	ADL27709	Mouse Fas cDNA, an
C 258	20	0.8	20	1	ADMS3428	Human Fas antisense	C 331	16.8	0.7	20	1	ADM53481	Mouse Fas antisense
C 259	20	0.8	20	1	ADMS3434	Human Fas antisense	C 332	16.8	0.7	20	1	ADO46746	Human oligonucleot
C 260	20	0.8	20	1	ADMS3533	Human Fas antisense	C 333	16.8	0.7	21	1	AAZ72477	Human biallelic ma
C 261	20	0.8	20	1	ADMS3537	Human Fas antisense	C 334	16.8	0.7	21	1	AAZ76741	Human ILs-R oligon
C 262	20	0.8	20	1	ADMS3540	Human Fas antisense	C 335	16.4	0.6	19	1	ABZ97640	Human ILs-R derive
C 263	20	0.8	20	1	ADMS3544	Human Fas antisense	C 336	16.4	0.6	19	1	ABD30671	Oligonucleotide as
C 264	20	0.8	20	1	ADMS3546	Human Fas antisense	C 337	16.4	0.6	19	1	ADJ59461	Human oligonucleot
C 265	20	0.8	20	1	ADMS3552	Human Fas antisense	C 338	16.4	0.6	19	1	ADJ59461	Oligonucleotide as
C 266	20	0.8	20	1	ADMS3557	Human Fas antisense	C 339	15.8	0.6	19	1	ADJ59461	Mitogen activated
C 267	20	0.8	20	1	ADMS3557	Human Fas antisense	C 340	15.8	0.6	19	1	ADJ59461	Mitogen activated
C 268	20	0.8	20	1	ADMS3557	Human Fas antisense	C 341	15.4	0.6	17	1	AAZ76741	Hammerhead ribozym
C 269	20	0.8	20	1	ADMS3531	Human Fas antisense	C 342	15.4	0.6	17	1	AAZ76741	Hammerhead ribozym
C 270	20	0.8	20	1	ADMS3532	Human Fas antisense	C 343	15.4	0.6	17	1	AAZ76741	Hammerhead ribozym
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C 272	20	0.8	20	1	ADMS3532	Human Fas antisense	C 345	15.4	0.6	18	1	AAZ76741	U. urealyticum det
C 273	20	0.8	20	1	ADMS3419	Human Fas antisense	C 346	15.4	0.6	19	1	AAZ76741	Cdc 25 hs ribozyme
C 274	20	0.8	20	1	ADMS3423	Human Fas antisense	C 347	15.4	0.6	19	1	AAZ76741	Cdc 25 hs ribozyme
C 275	20	0.8	20	1	ADMS3551	Human Fas antisense	C 348	15.4	0.6	19	1	AAZ76741	Cdc25 hs ribozyme
C 276	20	0.8	20	1	ADMS3432	Human Fas antisense	C 349	15.4	0.6	19	1	AAZ76741	Cdc25 hs ribozyme
C 277	20	0.8	20	1	ADMS3519	Human Fas antisense	C 350	15	0.6	15	1	AAZ76741	Human Fas antigen
C 278	20	0.8	20	1	ADMS3521	Human Fas antisense	C 351	15	0.6	15	1	AAZ76741	Human Fas antigen
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C 285	20	0.8	20	1	ADMS3530	Human Fas antisense	C 358	14.4	0.6	17	1	AAZ76741	Oligonucleotide as
C 286	20	0.8	20	1	ADMS3531	Human Fas antisense	C 359	14.4	0.6	17	1	AAZ76741	Oligonucleotide as
C 287	20	0.8	20	1	ADMS3534	Human Fas antisense	C 360	14.4	0.6	17	1	AAZ76741	Oligonucleotide as
C 288	20	0.8	20	1	ADMS3535	Human Fas antisense	C 361	14.4	0.6	17	1	AAZ76741	Oligonucleotide as
C 289	20	0.8	20	1	ADMS3536	Human Fas antisense	C 362	14.4	0.6	17	1	AAZ76741	Oligonucleotide as
C 290	20	0.8	20	1	ADMS3537	Human Fas antisense	C 363	14.4	0.6	17	1	AAZ76741	Oligonucleotide as
C 291	20	0.8	20	1	ADMS3538	Human Fas antisense	C 364	14.4	0.6	17	1	AAZ76741	Oligonucleotide as
C 292	20	0.8	20	1	ADMS3539	Human Fas antisense	C 365	14.4	0.6	17	1	AAZ76741	Oligonucleotide as
C 293	20	0.8	20	1	ADMS3540	Human Fas antisense	C 366	14.4	0.6	17	1	AAZ76741	Oligonucleotide as
C 294	20	0.8	20	1	ADMS3541	Human Fas antisense	C 367	14.4	0.6	17	1	AAZ76741	Oligonucleotide as
C 295	20	0.8	20	1	ADMS3542	Human Fas antisense	C 368	14.4	0.6	17	1	AAZ76741	Oligonucleotide as
C 296	20	0.8	20	1	ADMS3543	Human Fas antisense	C 369	14.4	0.6	17	1	AAZ76741	Oligonucleotide as
C 297	20	0.8	20	1	ADMS3544	Human Fas antisense	C 370	14.4	0.6	17	1	AAZ76741	Oligonucleotide as
C 298	20	0.8	20	1	ADMS3545	Human Fas antisense	C 371	14.4	0.6	17	1	AAZ76741	Oligonucleotide as
C 299	20	0.8	20	1	ADMS3546	Human Fas antisense	C 372	14.4	0.6	17	1	AAZ76741	Oligonucleotide as
C 300	20	0.8	20	1	ADMS3547	Human Fas antisense	C 373	14.4	0.6	17	1	AAZ76741	Oligonucleotide as
C 301	20	0.8	20	1	ADMS3548	Human Fas antisense	C 374	14.4	0.6	17	1	AAZ76741	Oligonucleotide as
C 302	20	0.8	20	1	ADMS3549	Human Fas antisense	C 375	14.4	0.6	17	1	AAZ76741	Oligonucleotide as
C 303	20	0.8	20	1	ADMS3550	Human Fas antisense	C 376	14.4	0.6	17	1	AAZ76741	Oligonucleotide as
C 304	20	0.8	20	1	ADMS3551	Human Fas antisense	C 377	14.4	0.6	17	1	AAZ76741	Oligonucleotide as
C 305	20	0.8	20	1	ADMS3552	Human Fas antisense	C 378	14.4	0.6	17	1	AAZ76741	Oligonucleotide as
C 306	20	0.8	20	1	ADMS3553	Human Fas antisense	C 379	14.4	0.6	17	1	AAZ76741	Oligonucleotide as
C 307	20	0.8	20	1	ADMS3554	Human Fas antisense	C 380	14.4	0.6	17	1	AAZ76741	Oligonucleotide as
C 308	20	0.8	20	1	ADMS3555	Human Fas antisense	C 381	14.4	0.6	17	1	AAZ76741	Oligonucleotide as
C 309	20	0.8	20	1	ADMS3556	Human Fas antisense	C 382	14.4	0.6	17	1	AAZ76741	Oligonucleotide as
C 310	20	0.8	20	1	ADMS3557	Human Fas antisense	C 383	14.4	0.6	17	1	AAZ76741	Oligonucleotide as
C 311	20	0.8	20	1	ADMS3558	Human Fas antisense	C 384	14.4	0.6	17	1	AAZ76741	Oligonucleotide as
C 312	20	0.8	20	1	ADMS3559	Human Fas antisense	C 385	14.4	0.6	17	1	AAZ76741	Oligonucleotide as
C 313	20	0.8	20	1	ADMS3560	Human Fas antisense	C 386	14.4	0.6	17	1	AAZ76741	Oligonucleotide as
C 314	20	0.8	20	1	ADMS3561	Human Fas antisense	C 387	14.4	0.6	17	1	AAZ76741	Oligonucleotide as
C 315	20	0.8	20	1	ADMS3562	Human Fas antisense	C 388	14.4	0.6	17	1	AAZ76741	Oligonucleotide as
C 316	20	0.8	20	1	ADMS3563	Human Fas antisense	C 389	14.4	0.6	17	1	AAZ76741	Oligonucleotide as
C 317	20	0.8	20	1	ADMS3564	Human Fas antisense	C 390	14.4	0.6	17	1	AAZ76741	Oligonucleotide as
C 318	20	0.8	20	1	ADMS3565	Human Fas antisense	C 391	14.4	0.6	17	1	AAZ76741	Oligonucleotide as
C 319	20	0.8	20	1	ADMS3566	Human Fas antisense	C 392	14.4	0.6	17	1	AAZ76741	Oligonucleotide as
C 320	20	0.8	20	1	ADMS3567	Human Fas antisense	C 393	14.4	0.6	17	1	AAZ76741	Oligonucleotide as
C 321	20	0.8	20	1	ADMS3568	Human Fas antisense	C 394	14.4	0.6	17	1	AAZ76741	Oligonucleotide as
C 322	20	0.8	20	1	ADMS3569	Human Fas antisense	C 395	14.4	0.6	17	1	AAZ76741	Oligonucleotide as
C 323	20	0.8	20	1	ADMS3570	Human Fas antisense	C 396	14.4	0.6	17	1	AAZ76741	Oligonucleotide as
C 324	20	0.8	20	1	ADMS3571	Human Fas antisense	C 397	14.4	0.6	17	1	AAZ76741	Oligonucleotide as
C 325	20	0.8	20	1	ADMS3572	Human Fas antisense	C 398	14.4	0.6	17	1	AAZ76741	Oligonucleotide as

Human caspase-8 an
Human infertility
PCR primer used to
Oligonucleotide as
Oligonucleotide as
Mouse Fas cDNA, an
Mouse Fas antisense
Human oligonucleot
Human biallelic ma
Human ILs-R oligon
Human ILs-R derive
Human oligonucleot
Human oligonucleot
Mitogen activated
Mitogen activated
Hammerhead ribozym
Hammerhead ribozym
Human G-alpha-i2 a
U. urealyticum det
Cdc 25 hs ribozyme
Cdc 25 hs ribozyme
Cdc25 hs ribozyme
Cdc25 hs ribozyme
Human Fas antigen
Human Fas antigen
Human Fas antigen
Human Fas antigen
Human Fas antigen
Human Fas antigen
Oligonucleotide as
Oligonucleotide as
Oreochromis niloti
Chicken THR9 prime
PCR primer used to
Hammerhead ribozym
Hammerhead ribozym
Hammerhead ribozym
Hammerhead ribozym
Waxy starch produc
Waxy starch produc
WNV minus strand H
WNV minus strand H
WNV Hammerhead Rib
WNV Hammerhead Rib
WNV minus strand I
WNV minus strand I
Tumour suppression
Tumour suppression
Murine oligonucleo
Murine oligonucleo
Murine oligonucleo
Murine oligonucleo
Human breast cance
Tumour suppression
Human Na/H exchang
Human Na/H exchang
Tumour suppression
Tumour suppress
Human tumour suppr
Human tumour suppr
Mutant cell identi
Mutant cell identi
Poly nucleotide dir
Synthetic deoxyrib
Human SRC-3 antise
Human SRC-3 antise
Poly y nucleotide
Probe poly y for a
Human cyclin-depen
IGFBP3 oligonucleo
IGFBP3 oligonucleo
IGFBP3 oligonucleo
IGFBP3 oligonucleo
Probe #69 used to
Human TIE-2 substr
Hammerhead ribozym
Human ERG hammerhe
Human ERG hammerhe
Human ERG hammerhe
Murine oligonucleo
Tumour suppression

C 399	14	0.5	17	1	ADB45339	Tumour suppression
C 400	13.8	0.5	17	1	AAQ22152	Sequencing primer
C 401	13.8	0.5	17	1	AAV70126	Human flt1 VEGF re
C 402	13.8	0.5	17	1	AAV95875	Solanidine glucosyl
C 403	13.8	0.5	17	1	AAZ25585	Human RhoG PCR rev
C 404	13.8	0.5	17	1	AAZ20676	Integrin alpha 6 s
C 405	13.8	0.5	17	1	AAAI9042	Human IIE-2 substr
C 406	13.8	0.5	17	1	AAAI9041	Human IIE-2 substr
C 407	13.8	0.5	17	1	AAV91408	Human C-raf target
C 408	13.8	0.5	17	1	AAV59707	Antisense oligonuc
C 409	13.8	0.5	17	1	AAZ99788	Respiratory syncyt
C 410	13.8	0.5	17	1	AAZ99771	Nucleotide sequenc
C 411	13.8	0.5	17	1	AAA25314	Oestrogen receptor
C 412	13.8	0.5	17	1	AAA25315	Oestrogen receptor
C 413	13.8	0.5	17	1	AAAC87855	Bacillus thuringie
C 414	13.8	0.5	17	1	AAAF03120	Hammerhead ribozym
C 415	13.8	0.5	17	1	AAAF05433	Hammerhead ribozym
C 416	13.8	0.5	17	1	AAAF07470	Hammerhead ribozym
C 417	13.8	0.5	17	1	AAAF03119	Hammerhead ribozym
C 418	13.8	0.5	17	1	AAAF07471	Human NCOG Zinzyme
C 419	13.8	0.5	17	1	ABK01973	Human CD20 G-cleav
C 420	13.8	0.5	17	1	ABK03410	Alternative glucan
C 421	13.8	0.5	17	1	AAAS00805	Human GMPLP-1 17-m
C 422	13.8	0.5	17	1	ABN08319	Stress tolerance c
C 423	13.8	0.5	17	1	ABK25667	Increased stearate
C 424	13.8	0.5	17	1	ABK27004	Stress tolerance c
C 425	13.8	0.5	17	1	ABK27003	Increased stearate
C 426	13.8	0.5	17	1	ABK25668	Stress tolerance c
C 427	13.8	0.5	17	1	ABV90689	Human POSHL1 scann
C 428	13.8	0.5	17	1	ABK57249	Human CUCAL Gene e
C 429	13.8	0.5	17	1	ACN05702	WNV Amberzyme subs
C 430	13.8	0.5	17	1	ACN09214	WNV minus strand H
C 431	13.8	0.5	17	1	ACD00673	G-protein coupled
C 432	13.8	0.5	17	1	ACD00674	G-protein coupled
C 433	13.8	0.5	17	1	ABT32525	Tumour suppression
C 434	13.8	0.5	17	1	ABT32515	Tumour suppression
C 435	13.8	0.5	17	1	ABT32622	Tumour suppression
C 436	13.8	0.5	17	1	ABT32622	Tumour suppression
C 437	13.8	0.5	17	1	ABT37152	Tumour suppression
C 438	13.8	0.5	17	1	ABZ61647	Human H-Ras DNazym
C 439	13.8	0.5	17	1	ABZ60725	Human K-Ras DNazym
C 440	13.8	0.5	17	1	ABZ60258	Human K-Ras DNazym
C 441	13.8	0.5	17	1	ABZ60304	Human K-Ras DNazym
C 442	13.8	0.5	17	1	ACDS3115	HBV inozyme substr.
C 443	13.8	0.5	17	1	ACC63230	Murine oligonucleo
C 444	13.8	0.5	17	1	ACF04371	Respiratory syncyt
C 445	13.8	0.5	17	1	ACF04360	Respiratory syncyt
C 446	13.8	0.5	17	1	ADB41782	Tumour suppression
C 447	13.8	0.5	17	1	ADB40928	Tumour suppression
C 448	13.8	0.5	17	1	ADC04388	Human Na/H exchang
C 449	13.8	0.5	17	1	ADC04389	Human Na/H exchang
C 450	13.8	0.5	17	1	ADB44312	Tumour suppression
C 451	13.8	0.5	17	1	ADI47563	Human tumour suppr
C 452	13.8	0.5	17	1	ADI47582	Human tumour suppr
C 453	13.8	0.5	17	1	ADI49040	Human tumour suppr
C 454	13.8	0.5	17	1	ADI51786	Human tumour suppr
C 455	13.8	0.5	17	1	ADI49027	Human tumour suppr
C 456	13.8	0.5	17	1	ADI50416	Human tumour suppr
C 457	13.8	0.5	17	1	ADI52708	Human tumour suppr
C 458	13.8	0.5	17	1	ADI47806	Human tumour suppr
C 459	13.8	0.5	17	1	ACC54404	Human tumour suppr
C 460	13.8	0.5	17	1	ACC53225	Human tumour suppr
C 461	13.8	0.5	17	1	ADL49542	Human PKR substrat
C 462	13.8	0.5	17	1	ADK13132	Human glioma endot
C 463	13.8	0.5	17	1	ADL82276	Human ER+ breast c
C 464	13.8	0.5	17	1	ADM59302	Hepatitis B virus
C 465	13.8	0.5	17	1	ADM60057	Mutant cell identi
C 466	13.8	0.5	17	1	ADN44358	Mutant cell identi
C 467	13.8	0.5	17	1	ADN44359	Mutant cell identi
C 468	13.8	0.5	17	1	ADN45695	Mutant cell identi
C 469	13.8	0.5	17	1	ADN45694	Human plx1 antisen
C 470	13.8	0.5	17	1	AQ226937	Human Acetylcholin
C 471	13.6	0.5	15	1	AA596167	

47213.60.5151ABK81472Human CASP5 gene a

ALIGNMENTS

RESULT 1

ABZ00256 standard; DNA; 50 BP.

XX

AC

ABZ00256;

XX

09-JAN-2003 (first entry)

XX

Human leukocyte gene expression profiling probe SEQ ID NO 247.

DE

XX

T7; leukocyte; gene expression profiling; allograft rejection;

KW

atherosclerosis; congestive heart failure; systemic lupus erythematosus;

KW

rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;

XX

ss.

XX

Homo sapiens.

OS

XX

WO200257414-A2.

PN

XX

25-JUL-2002.

PD

XX

22-OCT-2001; 2001WO-US047856.

PF

XX

20-OCT-2000; 2000US-0241994P.

PR

XX

08-JUN-2001; 2001US-0296764P.

PR

XX

(BIOC-) BIOCARDIA INC.

PA

XX

Wohlgemuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;

PI

Ly N, Woodward R, Quattermous T, Johnson F;

PI

XX

WPI; 2002-638525/68.

XX

New system for leukocyte expression profiling, diagnosing a disease, or

PT

monitoring (the rate of) progression of a disease, e.g. atherosclerosis

PT

or congestive heart failure, comprises diagnostic oligonucleotides.

XX

Claim 1; Page 334; Opp; English.

PS

XX

The invention relates to a system for detecting gene expression, which

CC

comprises one or two isolated DNA molecules that detect expression of a

CC

gene, where the gene corresponds to any of 8143 oligonucleotides

CC

(ABZ0010-ABZ08152) each having 50 base pairs (bp). The system is useful

CC

for leukocyte expression profiling. It is particularly useful for

CC

diagnosing a disease, monitoring (rate of) progression of a disease,

CC

predicting therapeutic outcome, determining prognosis for a patient,

CC

predicting disease complications in an individual or monitoring response

CC

to treatment in an individual. The diseases include cardiac allograft

CC

rejection, kidney allograft rejection, liver allograft rejection,

CC

atherosclerosis, congestive heart failure, systemic lupus erythematosus,

CC

rheumatoid arthritis, osteoarthritis or cytomegalovirus infection

XX

Sequence 50 BP; 13 A; 12 C; 7 G; 18 T; 0 U; 0 Other;

XX

Query Match 2.0%; Score 50; DB 1; Length 50;

Best Local Similarity 100.0%; Pred. No. 0.45; Length 50;

Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

2273 AATCATCATCTCGATTAGGAATTCCTTCTGTCATACCCCAAGTTCTTA 2322

DB

1 AATCATCATCTCGATTAGGAATTCCTTCTGTCATACCCCAAGTTCTTA 50

RESULT 2

ABZ03786

ID

ABZ03786 standard; DNA; 50 BP.

XX

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2004, 14:05:51 ; Search time 6 Seconds
(without alignments)
3.457 Million cell updates/sec

Title: US-10-619-220-1
Perfect score: 2551
Sequence: 1 gcaagagtacacacaggtg.....taaaagtacgraattaaata 2551

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 207 seqs, 4066 residues

Total number of hits satisfying chosen parameters: 414

Minimum DB seq length: 8
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 213 summaries

Database : rni1.seq:
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	39.4	1.5	45	1	US-08-339-214-87
C 2	38.4	1.5	45	1	US-08-339-214-86
C 3	34.6	1.4	41	1	US-08-444-231-2
C 4	34.6	1.4	41	1	US-08-152-443A-2
C 5	33	1.3	41	1	US-08-444-231-1
C 6	33	1.3	41	1	US-08-152-443A-1
C 7	32	1.3	32	1	US-08-859-998-385
C 8	32	1.3	32	1	US-09-225-928-385
C 9	32	1.3	32	1	US-09-225-201B-385
C 10	31	1.2	31	1	US-09-665-615B-90
C 11	30.4	1.2	32	1	US-08-859-998-386
C 12	30.4	1.2	32	1	US-09-225-928-386
C 13	30.4	1.2	32	1	US-09-225-201B-386
C 14	29	1.1	29	1	US-09-665-615B-88
C 15	27	1.1	27	1	US-08-444-231-10
C 16	27	1.1	27	1	US-08-152-443A-10
C 17	26	1.0	26	1	US-08-444-231-9
C 18	26	1.0	26	1	US-08-152-443A-9
C 19	26	1.0	26	1	US-09-665-615B-89
C 20	24	0.9	24	1	US-08-322-805-2
C 21	24	0.9	24	1	US-08-429-499-2
C 22	24	0.9	24	1	US-09-152-733-2
C 23	24	0.9	24	1	US-08-339-214-39
C 24	24	0.9	24	1	US-09-481-620A-120
C 25	21	0.8	21	1	US-08-713-557B-8
C 26	21	0.8	21	1	PCT-US95-17083-11
C 27	20.8	0.8	24	1	US-08-444-005-7
C 28	20.8	0.8	24	1	US-08-444-005-8
C 29	20	0.8	20	1	US-09-290-640-3
C 30	20	0.8	20	1	US-09-290-640-4
C 31	20	0.8	20	1	US-09-290-640-5
C 32	20	0.8	20	1	US-09-290-640-6
C 33	20	0.8	20	1	US-09-290-640-7

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Sequence 9, Appli	20	0.8	20	1	US-09-290-640-9
Sequence 10, Appli	20	0.8	20	1	US-09-290-640-10
Sequence 11, Appli	20	0.8	20	1	US-09-290-640-11
Sequence 12, Appli	20	0.8	20	1	US-09-290-640-12
Sequence 13, Appli	20	0.8	20	1	US-09-290-640-13
Sequence 14, Appli	20	0.8	20	1	US-09-290-640-14
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Sequence 18, Appli	20	0.8	20	1	US-09-290-640-18
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Sequence 20, Appli	20	0.8	20	1	US-09-290-640-20
Sequence 21, Appli	20	0.8	20	1	US-09-290-640-21
Sequence 22, Appli	20	0.8	20	1	US-09-290-640-22
Sequence 23, Appli	20	0.8	20	1	US-09-290-640-23
Sequence 3, Appli	20	0.8	20	1	US-09-665-615B-3
Sequence 4, Appli	20	0.8	20	1	US-09-665-615B-4
Sequence 5, Appli	20	0.8	20	1	US-09-665-615B-5
Sequence 6, Appli	20	0.8	20	1	US-09-665-615B-6
Sequence 7, Appli	20	0.8	20	1	US-09-665-615B-7
Sequence 8, Appli	20	0.8	20	1	US-09-665-615B-8
Sequence 9, Appli	20	0.8	20	1	US-09-665-615B-9
Sequence 10, Appli	20	0.8	20	1	US-09-665-615B-10
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Sequence 16, Appli	20	0.8	20	1	US-09-665-615B-16
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Sequence 18, Appli	20	0.8	20	1	US-09-665-615B-18
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Sequence 22, Appli	20	0.8	20	1	US-09-665-615B-22
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Sequence 118, App	20	0.8	20	1	US-09-665-615B-118
Sequence 119, App	20	0.8	20	1	US-09-665-615B-119
Sequence 120, App	20	0.8	20	1	US-09-665-615B-120
Sequence 121, App	20	0.8	20	1	US-09-665-615B-121
Sequence 122, App	20	0.8	20	1	US-09-665-615B-122
Sequence 123, App	20	0.8	20	1	US-09-665-615B-123
Sequence 124, App	20	0.8	20	1	US-09-665-615B-124
Sequence 125, App	20	0.8	20	1	US-09-665-615B-125
Sequence 126, App	20	0.8	20	1	US-09-665-615B-126
Sequence 127, App	20	0.8	20	1	US-09-665-615B-127
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Sequence 129, App	20	0.8	20	1	US-09-665-615B-129
Sequence 130, App	20	0.8	20	1	US-09-665-615B-130
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Patent No. 5182195

ALIGNMENTS

RESULT 1
US-08-339-214-87/c
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; Patent No. 6348334
; GENERAL INFORMATION:
; APPLICANT: Nagata, Shigikazu
; APPLICANT: Suda, Takashi
; APPLICANT: Takahashi, Tomonori
; APPLICANT: Nakamura, No. 6348334
; TITLE OF INVENTION: A Fas Ligand, A Fragment Thereof and DNA
; TITLE OF INVENTION: Encoding the Same
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/339,214
; FILING DATE: 10-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy Jr., Gerald M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1110-139P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000

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OM nucleic - nucleic search, using sw model

Run on: October 27, 2004, 14:07:41 ; Search time 6 Seconds
(without alignments)

4.082 Million cell updates/sec

Title: US-10-619-220-1

Perfect score: 2551

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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 0.5

Searched: 241 seqs, 4801 residues

Total number of hits satisfying chosen parameters: 482

Minimum DB seq length: 8

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 241 summaries

Database : rnpb1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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6	30.6	1.2	31	1	US-09-912-263-249	Sequence 249, App
7	29	1.1	29	1	US-09-802-669-88	Sequence 88, Appl
8	29	1.1	29	1	US-10-619-220-88	Sequence 88, Appl
C 9	26	1.0	26	1	US-09-802-669-89	Sequence 89, Appl
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11	25	1.0	25	1	US-09-814-699-1	Sequence 1, Appl
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14	24	0.9	24	1	US-10-741-601-26410	Sequence 26410, A
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EcoRI R. Site 2: NotI Description: Normalised library constructed
from pooled tissue from day 30 placentas. Clones available from UK
Centre for Functional Genomics in Farm Animals, Roslin Institute,
Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.

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Best Local Similarity 89.5%; Pred. No. 0.52;
Matches 17; Conservative 2; Indels 0; Gaps 0;
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Db 19 TTTTTCCTCCACCCCC 1

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DEFINITION E012394-024-013-B09-SP6 MP12-ADIS-024-leaf Beta vulgaris cDNA clone
024-013-B09 5-PRIME, mRNA sequence.
ACCESSION BQ586069
VERSION BQ586069.1 GI:26115651
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.

REFERENCE 1 (bases 1 to 18)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruock,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698

COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
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b.schulz@kws.de; cloning sites Sall-NotI, primer sites and

FEATURES
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b.schulz@kws.de; cloning sites Sall-NotI, primer sites and

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OM nucleic - nucleic search, using sw model
Run on: October 27, 2004, 14:09:36 ; Search time 0.001 Seconds
(without alignments)
418.364 Million cell updates/sec

Title: US-10-619-220-1
Perfect score: 2551
Sequence: 1 gcaagagtgacacacagtg.....taaaagtacgtaataaata 2551

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 0.5
Searched: 5 seqs, 82 residues
Total number of hits satisfying chosen parameters: 10

Minimum DB seq length: 8
Maximum DB seq length: 50
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 5 summaries

Database: rst1.seq.*
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES				
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C 2	15	0.6	18 1	BQ586069 ACCESSION:BQ586069
C 3	14.4	0.6	17 1	AJ592533 ACCESSION:AJ592533
C 4	12.4	0.5	14 1	AJ58636 ACCESSION:AJ58636
C 5	12.4	0.5	14 1	AJ597309 ACCESSION:AJ597309

ALIGNMENTS

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LOCUS AJ666296 19 bp mRNA linear EST 28-JUN-2004
DEFINITION AJ666296 CSEQRAN09 Sus scrofa cDNA clone C0000033_B06, mRNA
sequence.
ACCESSION AJ666296
VERSION AJ666296.1 GI:49350747
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
TITLE Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
JOURNAL Unpublished (2004)
COMMENT Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
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C 157	20	0.8	20	1	US-10-619-220-60	Sequence 60, Appl	Sequence 60, Appl
C 158	20	0.8	20	1	US-10-619-220-61	Sequence 61, Appl	Sequence 61, Appl
C 159	20	0.8	20	1	US-10-619-220-62	Sequence 62, Appl	Sequence 62, Appl
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C 162	20	0.8	20	1	US-10-619-220-65	Sequence 65, Appl	Sequence 65, Appl
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C 178	20	0.8	20	1	US-10-619-220-81	Sequence 81, Appl	Sequence 81, Appl
C 179	20	0.8	20	1	US-10-619-220-82	Sequence 82, Appl	Sequence 82, Appl

ALIGNMENTS

RESULT 1
US-10-131-827-247
Sequence 247, Application US/10131827
Publication No. US20040009479A1
GENERAL INFORMATION:
APPLICANT: Wohlgenuth, Jay

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 27, 2004, 14:12:21 ; Search time 0.001 Seconds
(without alignments)
56.200 Million cell updates/sec

Title: US-10-619-220-73

Perfect score: 20

Sequence: 1 tccagcactttctttccgg 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 130 seqs, 1405 residues

Total number of hits satisfying chosen parameters: 260

Minimum DB seq length: 8

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 130 summaries

Database : rge73.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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24	10	50.0	12	1	I72094
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28	10	50.0	12	1	I72116
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1	CO836350	11	45.0	9	C 49
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ALIGNMENTS

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DEFINITION Sequence 73 from patent US 6204055.
ACCESSION AR143179
VERSION AR143179.1 GI:15104465
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dean,N.M., and Marcussen,E.G.
TITLE Antisense inhibition of Fas mediated signaling
JOURNAL Patent: US 6204055-A 73 20-MAR-2001;
FEATURES Location/Qualifiers
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Db 1 TCCAGCACTTCTTTTCGG 20

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LOCUS BD249354 20 bp DNA linear PAT 17-JUL-2003
DEFINITION Antisense modulation of Fas mediated signaling.
ACCESSION BD249354
VERSION BD249354.1 GI:33059124
KEYWORDS JP 2002540812-A/69.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dean,N.M. and Marcussen,E.G.
TITLE Antisense modulation of Fas mediated signaling
JOURNAL Patent: JP 2002540812-A 69 03-DEC-2002;
COMMENT ISIS PHARMACEUTICALS INC
CS Artificial Sequence

PN JP 2002540812-A/69
PD 03-DEC-2002
PR 10-APR-2000 JP 2000610483
PI NICHOLAS M DEAN,ERIC G MARCUSSON
PC C12N15/09,A61K31/7088,A61K31/7115,A61K31/712,A61K31/7125, PC
A61K48/00,
PC A61P1/16,A61P29/00,A61P35/00,A61P37/00,A61P43/00//C12N5/06, PC
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DEFINITION Sequence 73 from patent US 6653133.
ACCESSION AR432273
VERSION AR432273.1 GI:40194546
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dean,N.M., Marcussen,E.G. and Wyatt,J.
TITLE Antisense modulation of Fas mediated signaling
JOURNAL Patent: US 6653133-A 73 25-NOV-2003;
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RESULT 4
LOCUS I38970 15 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 8 from patent US 5616488.
ACCESSION I38970
VERSION I38970.1 GI:2083450
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Sullivan,S., Draper,K.G., McSwiggen,J. and Stinchcomb,D.T.
TITLE IL-5 targeted ribozymes
JOURNAL Patent: US 5616488-A 8 01-APR-1997;
FEATURES Location/Qualifiers
source 1..15

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OM nucleic - nucleic search, using sw model

Run on: October 27, 2004, 14:19:47 ; Search time 0.001 Seconds
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103.800 Million cell updates/sec

Title: US-10-619-220-73

Perfect score: 20

Sequence: 1 tccagcactttctttccgg 20

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 0.5

Searched: 238 seqs, 2595 residues

Total number of hits satisfying chosen parameters: 476

Minimum DB seq length: 8

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 238 summaries

Database : rng73.seq*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	20	100.0	20	1	Mouse Fas cDNA, an
6	20	100.0	20	1	Mouse Fas antisens
7	12.4	62.0	15	1	Human IL-5 hamme
8	12.4	62.0	15	1	Human IL-5 hamme
9	11.4	57.0	13	1	CFTR gene associat
10	11.4	57.0	13	1	DNA array associat
11	11	55.0	12	1	Oligonucleotide pr
12	11	55.0	12	1	Oligonucleotide SE
13	11	55.0	12	1	Oligonucleotide SE
14	11	55.0	12	1	Oligonucleotide SE
15	11	55.0	12	1	Oligonucleotide SE
16	10.4	52.0	12	1	Oligonucleotide pr
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65	10	50.0	12	1	ABSV7226	Oligonucleotide pr
66	10	50.0	12	1	ABSV7226	Oligonucleotide pr
67	9.4	47.0	11	1	AAAS4619	Human P selectin D
68	9.4	47.0	11	1	AAAS4619	Human P selectin D
69	9.4	47.0	11	1	AAAS4619	Human P selectin D
70	9.4	47.0	11	1	AAAS4619	Human P selectin D
71	9.4	47.0	11	1	AAAS4619	Human P selectin D
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73	9.4	47.0	11	1	AAAS4619	Human P selectin D
74	9.4	47.0	11	1	AAAS4619	Human P selectin D
75	9.4	47.0	11	1	AAAS4619	Human P selectin D
76	9.4	47.0	11	1	AAAS4619	Human P selectin D
77	9.4	47.0	11	1	AAAS4619	Human P selectin D
78	9.4	47.0	11	1	AAAS4619	Human P selectin D
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80	9.4	47.0	11	1	AAAS4619	Human P selectin D
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C 107	8.4	42.0	10	1	AA14816	Triple helix formi
C 108	8.4	42.0	10	1	AA14766	Triple helix formi
C 109	8.4	42.0	10	1	AA02953	WO904041 Seq ID 6
C 110	8.4	42.0	10	1	AA277678	Human dendritic ce
C 111	8.4	42.0	10	1	AA278990	Human dendritic ce
C 112	8.4	42.0	10	1	AA278684	Human dendritic ce
C 113	8.4	42.0	10	1	AA278219	Human dendritic ce
C 114	8.4	42.0	10	1	AA283766	Metastatic breast
C 115	8.4	42.0	10	1	AA283450	Metastatic breast
C 116	8.4	42.0	10	1	AA281243	Metastatic breast
C 117	8.4	42.0	10	1	AA281950	Metastatic breast
C 118	8.4	42.0	10	1	AA283161	Metastatic breast
C 119	8.4	42.0	10	1	AA283175	Metastatic breast
C 120	8.4	42.0	10	1	AA281051	Metastatic breast
C 121	8.4	42.0	10	1	AA284388	Metastatic breast
C 122	8.4	42.0	10	1	AA285130	Metastatic breast
C 123	8.4	42.0	10	1	AA291581	Metastatic breast
C 124	8.4	42.0	10	1	AA291107	Human dendritic ce
C 125	8.4	42.0	10	1	AA291581	Human dendritic ce
C 126	8.4	42.0	10	1	AA286494	Human macrophage g
C 127	8.4	42.0	10	1	AA286419	Human macrophage g
C 128	8.4	42.0	10	1	AA283756	Human ubiquitously
C 129	8.4	42.0	10	1	AA284268	Human ubiquitously
C 130	8.4	42.0	10	1	AA283755	Human IGFA gene p
C 131	8.4	42.0	10	1	AA283126	LPS activated huma
C 132	8.4	42.0	10	1	AA2832738	Yeast NORF gene SA
C 133	8.4	42.0	10	1	AA283775	Yeast NORF gene SA
C 134	8.4	42.0	10	1	AA283616	Yeast NORF gene SA
C 135	8.4	42.0	10	1	AA284158	Yeast NORF gene SA
C 136	8.4	42.0	10	1	AA283857	Yeast NORF gene SA
C 137	8.4	42.0	10	1	AA2836214	Yeast NORF gene SA
C 138	8.4	42.0	10	1	AA283615	Yeast NORF gene SA
C 139	8.4	42.0	10	1	AA284041	Yeast NORF gene SA
C 140	8.4	42.0	10	1	AA2838491	Yeast NORF gene SA
C 141	8.4	42.0	10	1	AA2835093	Yeast NORF gene SA
C 142	8.4	42.0	10	1	AA283945	Yeast NORF gene SA
C 143	8.4	42.0	10	1	AA283986	Yeast NORF gene SA
C 144	8.4	42.0	10	1	AA2839649	Yeast NORF gene SA
C 145	8.4	42.0	10	1	AA283948	Yeast NORF gene SA
C 146	8.4	42.0	10	1	AA283952	Yeast NORF gene SA
C 147	8.4	42.0	10	1	AA283701	Yeast NORF gene SA
C 148	8.4	42.0	10	1	AA2835215	Yeast NORF gene SA
C 149	8.4	42.0	10	1	AA2836378	Yeast NORF gene SA
C 150	8.4	42.0	10	1	AA2836900	Primer-extension o
C 151	8.4	42.0	10	1	AA2842853	Human maturation/a
C 152	8.4	42.0	10	1	AA2842926	Human maturation/a
C 153	8.4	42.0	10	1	AA2841442	SCYA20 primer exte
C 154	8.4	42.0	10	1	AA2842882	Human GEM8 gene po
C 155	8.4	42.0	10	1	AA2843682	Human lysosomal ac
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C 157	8.4	42.0	10	1	AA2849429	DNA tag from human
C 158	8.4	42.0	10	1	AA2841709	Zinc finger protei
C 159	8.4	42.0	10	1	AA2840116	Human androgen-reg
C 160	8.4	42.0	10	1	AA2841473	Optineurin promote
C 161	8.4	42.0	10	1	AA2838629	Human CTFP gene al
C 162	8.4	42.0	10	1	AA2839969	Human TNFRSF1A gen
C 163	8.4	42.0	10	1	AA2842225	Human transcriptio
C 164	8.4	42.0	10	1	AA28475077	Photodamage detect
C 165	8.4	42.0	10	1	AA28475117	Photodamage detect
C 166	8.4	42.0	10	1	AA28475057	Photodamage detect
C 167	8.4	42.0	10	1	AA28477072	Photodamage marker
C 168	8.4	42.0	10	1	AA28477092	Photodamage marker
C 169	8.4	42.0	10	1	AA28477132	Photodamage marker
C 170	8.4	42.0	10	1	AA28474419	Human retinoblasto
C 171	8.4	42.0	10	1	AA2843248	Oligo SEQ ID 83, u
C 172	8.4	42.0	10	1	AA2839842	Androgen-regulated
C 173	8.4	42.0	10	1	AA28396028	Oligonucleotide #1
C 174	8.4	42.0	10	1	AA28396028	Human APC gene, -re
C 175	8.4	42.0	10	1	AA28396028	Peptide nucleic ac
C 176	8.4	42.0	10	1	AA28396028	Peptide nucleic ac
C 177	8.4	42.0	10	1	AA28396028	Peptide nucleic ac
C 178	8.4	42.0	10	1	AA28396028	Peptide nucleic ac
C 179	8.4	42.0	10	1	AA28396028	HIV-1 NL4-3 nef ge

ALIGNMENTS

RESULT 1
AAC61866
ID AAC61866 standard; DNA; 20 BP.
XX
AC AAC61866;
DT
XX 06-MAR-2001 (first entry)
XX
DE Antisense oligonucleotide directed against murine Fas (Apo-1) gene.

GenCore version S.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 27, 2004, 14:21:49 ; Search time 0.001 Seconds
(without alignments)
44.320 Million cell updates/sec

Title: US-10-619-220-73

Perfect score: 20

Sequence: 1 tccagcattttttccgg 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 106 seqs, 1108 residues

Total number of hits satisfying chosen parameters: 212

Minimum DB seq length: 8

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 106 summaries

Database : rni73.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	1	US-09-290-840-73
2	20	100.0	20	1	US-09-665-615B-73
3	12.4	62.0	15	1	US-08-319-492B-8
4	12.4	62.0	15	1	US-08-319-492B-8
5	11.4	57.0	13	1	US-08-544-381B-206
6	11.4	57.0	13	1	US-08-778-794A-15
7	11.4	57.0	13	1	US-08-341-399-15
8	10	50.0	12	1	US-08-004-800-9
9	10	50.0	12	1	US-08-004-800-10
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14	10	50.0	12	1	US-08-413-813-31
15	10	50.0	12	1	US-08-173-489C-215
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18	10	50.0	12	1	US-08-467-346-28
19	10	50.0	12	1	US-08-467-346-29
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33	8.4	42.0	10	1	US-09-508-753B-71
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8	40.0	10	1	US-08-150-156A-16	Sequence 16, Appl
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7	35.0	8	1	US-08-859-954-243	Sequence 243, App
7	35.0	8	1	US-08-859-954-421	Sequence 421, App
7	35.0	8	1	US-08-859-954-422	Sequence 422, App

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OM nucleic - nucleic search, using sw model

Run on: October 27, 2004, 14:23:56 ; Search time 0.001 Seconds
(without alignments)
22.320 Million cell updates/sec

Title: US-10-619-220-73
Perfect score: 20
Sequence: 1 tccagcactttcttttcgg 20
Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 50 seqs, 558 residues

Total number of hits satisfying chosen parameters: 100

Minimum DB seq length: 8
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : rnpb73.seq*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	20	100.0	20	1	US-09-803-669-73
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4	20	100.0	20	1	US-10-619-220-73
5	20	100.0	20	1	US-10-664-639A-114
6	11.4	57.0	13	1	US-09-510-378-206
7	11.4	57.0	13	1	US-09-798-260-15
8	10	50.0	11	1	US-10-450-797-170
9	9.4	47.0	11	1	US-10-450-797-547
10	9.4	47.0	11	1	US-10-450-797-973
11	9.4	47.0	11	1	US-10-645-187-9
12	9	45.0	10	1	US-09-979-593-58
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14	9	45.0	11	1	US-10-450-797-786
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18	8.4	42.0	10	1	US-10-033-145-1092
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33	8	40.0	10	1	US-09-955-410-12

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ALIGNMENTS

RESULT 1

US-09-799-848-25 ; Application US/09799848
; Sequence 25, Application US/09799848
; Patent No. US20010044145A1
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett
; APPLICANT: Cooke, Phillip
; APPLICANT: Crooke, Stanley
; APPLICANT: Wu, Hongjiang
; APPLICANT: Lima, Walter
; TITLE OF INVENTION: METHODS OF USING MAMMALIAN RNASE H AND COMPOSITIONS THEREOF
; FILE REFERENCE: ISPH-0521
; CURRENT APPLICATION NUMBER: US/09/799,848
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 09/343,809
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: US 09/684,254
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 09/203,716
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: US 60/067,458
; PRIOR FILING DATE: 1997-12-04
; PRIOR APPLICATION NUMBER: US 09/453,514
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 09/144,611
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: US 08/861,306
; PRIOR FILING DATE: 1997-04-21
; PRIOR APPLICATION NUMBER: US 08/244,993
; PRIOR FILING DATE: 1994-06-21
; PRIOR APPLICATION NUMBER: US 07/814,961
; PRIOR FILING DATE: 1991-12-24
; PRIOR APPLICATION NUMBER: US 09/462,280
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: PCT/US98/13966
; PRIOR FILING DATE: 1998-07-06
; PRIOR APPLICATION NUMBER: US 08/889,296
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: US 08/411,734
; PRIOR FILING DATE: 1995-04-03
; PRIOR APPLICATION NUMBER: US 08/007,996
; PRIOR FILING DATE: 1993-10-21
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 25
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Mus sp.
US-09-799-848-25

Query Match 100.0%; Score 20; DB 1; Length 20;

12472698
Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 11 Std Error: 0.00
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Seq primer: SP6.
Location/Qualifiers
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/db_xref="taxon:161934"
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SP6-Sali-CCACGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

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Query Match 47.0%; Score 9.4; DB 1; Length 11;
Best Local Similarity 30.9%; Fred. No. 0;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 47.0%; Score 9.4; DB 1; Length 11;
Best Local Similarity 30.9%; Fred. No. 0;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1 AACACTTCTT 11
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LOCUS DKFZP434J217.s1.434 (synonym: htes3) Homo sapiens cDNA clone
DEFINITION DKFZP434J217, mRNA sequence.
ACCESSION AL046337
VERSION AL046337.1 GI:49682663
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 8)
AUTHORS Koehrer, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
TITLE EST (Koehrer, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

QY 4 AGCACTTCTT 14
Db 1 AACACTTCTT 11
RESULT 2
AL046337 8 bp mRNA linear EST 06-JUL-2004
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DEFINITION DKFZP434J217, mRNA sequence.
ACCESSION AL046337
VERSION AL046337.1 GI:49682663
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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FEATURES
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FEATURES
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/clone="DKFZP434J217"
/tissue_type="testis"
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/note="Vector: pSport1; Site 1: Noti; Site 2: Sali"

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.
OM nucleic - nucleic search, using sw model
Run on: October 27, 2004, 14:26:08 ; Search time 0.001 Seconds
(without alignments)
2.360 Million cell updates/sec
Title: US-10-619-220-73
Perfect score: 20
Sequence: 1 tccagcactttctttccgg 20
Scoring table: IDENTITY.NUC
Gapop 10.0 , Gapext 0.5
Searched: 7 seqs, 59 residues
Total number of hits satisfying chosen parameters: 14
Minimum DB seq length: 8
Maximum DB seq length: 50
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 7 summaries
Database : rst73.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
SUMMARIES
Result No. Score Match length DB ID Description
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2 6.4 32.0 8 1 AL046337 ACCESSION:AL046337
3 6.4 32.0 8 1 CF277997 ACCESSION:CF277997
C 4 6.4 32.0 8 1 CF301888 ACCESSION:CF301888
C 5 6.4 32.0 8 1 CF302851 ACCESSION:CF302851
C 6 6.4 32.0 8 1 CF322818 ACCESSION:CF322818
7 6.4 32.0 8 1 CN763421 ACCESSION:CN763421

ALIGNMENTS
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DEFINITION S014678-024-030-006-SP6 MPIZ-ADIS-024-leaf Beta vulgaris cDNA clone
024-030-006 5-PRIME, mRNA sequence.
ACCESSION CF543159
VERSION CF543159.1 GI:34891599
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 11)
AUTHORS Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M., Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H. and Radelof, U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189

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CF543159 11 bp mRNA linear EST 22-SEP-2003
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ACCESSION CF543159
VERSION CF543159.1 GI:34891599
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
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